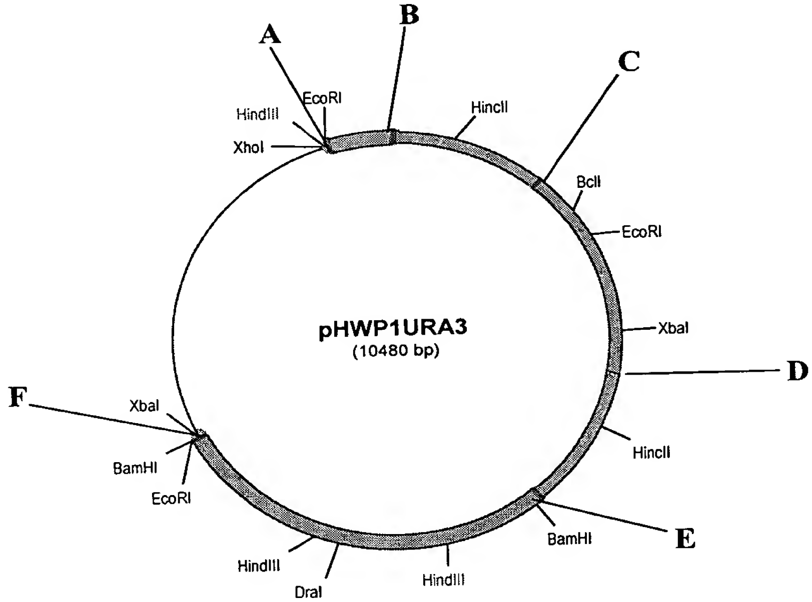

A
B
C
D
E
F
HindIII
EcoRI
XhoI
HincII
BclI
EcoRI
XbaI
HincII
BamHI
HindIII
DraI
HindIII
EcoRI
BamHI
XbaI
pHWP1URA3
(10480 bp)

Figure 1

Role of *HWP1* in health of mice orally colonized with *C. albicans*.

Mouse type	Health	Number of mice given *C. albicans* strains of *HWP1* type			
		I. **HWP1 HETEROZYGOTE**	*hwp1/hwp1** *homozygote*	II. **HWP1 REVERTANT**	Wild type
Beige nude	ill	5	2	3	3
	not ill	2	9	1	1
	total	7	11	4	4
	*P < 0.05 compared to the heterozygote, P = .058 compared to the revertant. P < .05 compared to combined heterozygote and revertant groups. Survival differences between other groups were not significant.				
Epsilon 26	ill	5	0	4	5
	Not ill	0	5	1	0
	total	5	5	5	5
	*P < .01 compared to individually to the heterozygote and revertant. groups. Survival differences between other groups were not significant.				

Figure 2

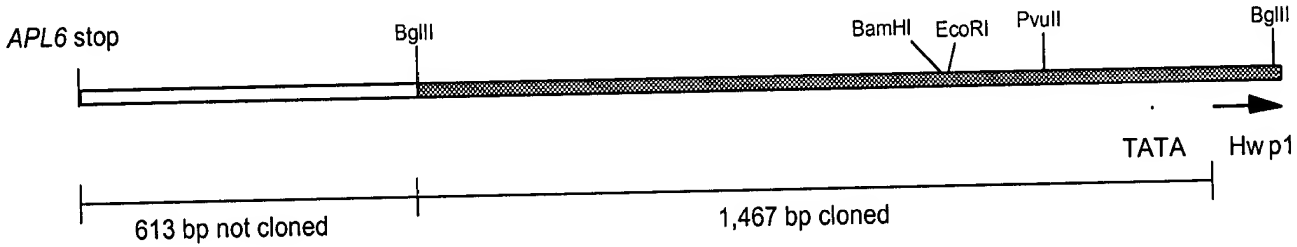


Figure 3

Figure 4

* * ◆ * *

GAT99 CTNCGTKTTPLWRRNPQGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRQR [SEQ ID. NO: 2]

:::: :.::::::::::.::::::::::::::::::::::::::::::::.:

NIT2 CTNCFTQTTPLWRRNPDGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRNR [SEQ ID. NO: 3]

Figure 5

TAATTCTAATAACTGATACTAAGTTTTGTTCCTTTTTTTGGGATTTCTTTTTTTTCTAATTTT
GATTGTTTTTCAATTTTGGGTTTTCAATATTATTGACAAGAGTCATTTTATTGAATATTTGT
TTTGTTTACTACATTAAAGGTGATAGGTACTTTTAGTTTTTAAAAATTGTTTTGTTCAAATT
GTTTATCTTTTTCTTCTTCTTCTACTTGCTTTGTTTTCTGTTTTCGGTTCATAGTTGATAGCTT
TT**AATAAA**TACCCCTTTTTTTTTACAATAGTTAGTTCTAAGCTTATTCAGTGGTTTAATTGG
TAGAAAATGTGAGCTCTGTAGCTTATGGTATCTTCTATAGCAATATATTTAACTTGGACAT
AGTTCATTATTCTGGACGCATGAAGGTGCAAAGTCAAAAAGTGAGAATATGCAAAGAGGT
AATTAGATTTCTGTCCTATTAATTAACAAAAAATC**TATATATA**GACTGCAATATTTAATAC
CCCCCAAGTTTGATTCTATAATCCTTCGATTTCTATAAAGATATAACCATGAATCATGAGT
AAATACCAAATAGATTAATAGTAGAATCTGTATGGTCGTGTAAAGCTGTTCATTAAAAAC
TATTGATTTAAATTTCCCCTTCCTCGTAATCTCTTTTTTTTTGGGGGGGAGGATCAGCCGCA
ATAAAAGATTGAAAATTATTAAACAAAACAACAAAACGGGAAACCGGAAACCTGAGAAA
AAGAAAGAAAGAAGGAAAACTTTTGTTAAGATATTAAATTTTACGAAGCAAATTTAAAAT
CCATACTTAACAATTATTGTTATTACGTACTTCAACAGGGAAAGAAAAAGTTAAGATTTTA
AATCTCTTTATTCCTTTCTTTCTTTTATTATTATTTACCCTTAATATAA***ATGTCAAAACAAGA***
TCCACCTCCAGATTATACAAATAGGACATCAGATAATTATAACCCAGATACAACTGATAATCA
TAATATTCCTCCACCTTTCACTACTCATCCTATAGAGGTTCATCCACCACCATTCTCCTCTTC
TACTTCACCTAATATCCGTGTGCCAGCATATTTTCAAAATCAAACTACTTCAGGATGGACAAT
AGTAATAAATAATCGATTTTGGACTGATGGATTCAGGATATTTGTTTCCGAAGATGCATCTAA
TAAGTTTGATGCCTTCAAAAAAAGTAAAAATCCCGAAATAATACAATTACAAGAACAAGGTA
TTGGAGTACCGTTATTTAAAGCTGTCACGTCATATATTCCCTTAGCAACAAAATTTATAACGT
TTAGAAGATATGTCCCTACTAATTTACATCCATTTGATATTGATAAAGATTATTATGATTATT
GTATTGTTAAACGGAAATTACACGTTGGATATGATAGTTATATATTTGAATTTACTCCTGATC
GAGAATTCGGATCC [SEQ ID. NO: 4]

Figure 6

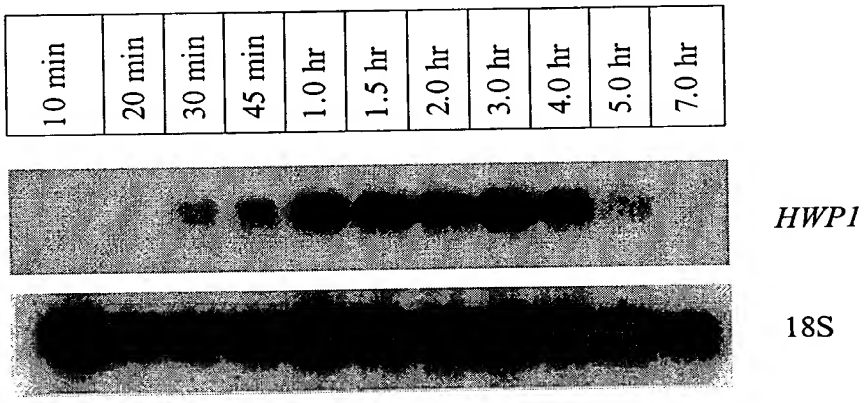

10 min
20 min
30 min
45 min
1.0 hr
1.5 hr
2.0 hr
3.0 hr
4.0 hr
5.0 hr
7.0 hr
HWP1
18S

Figure 7

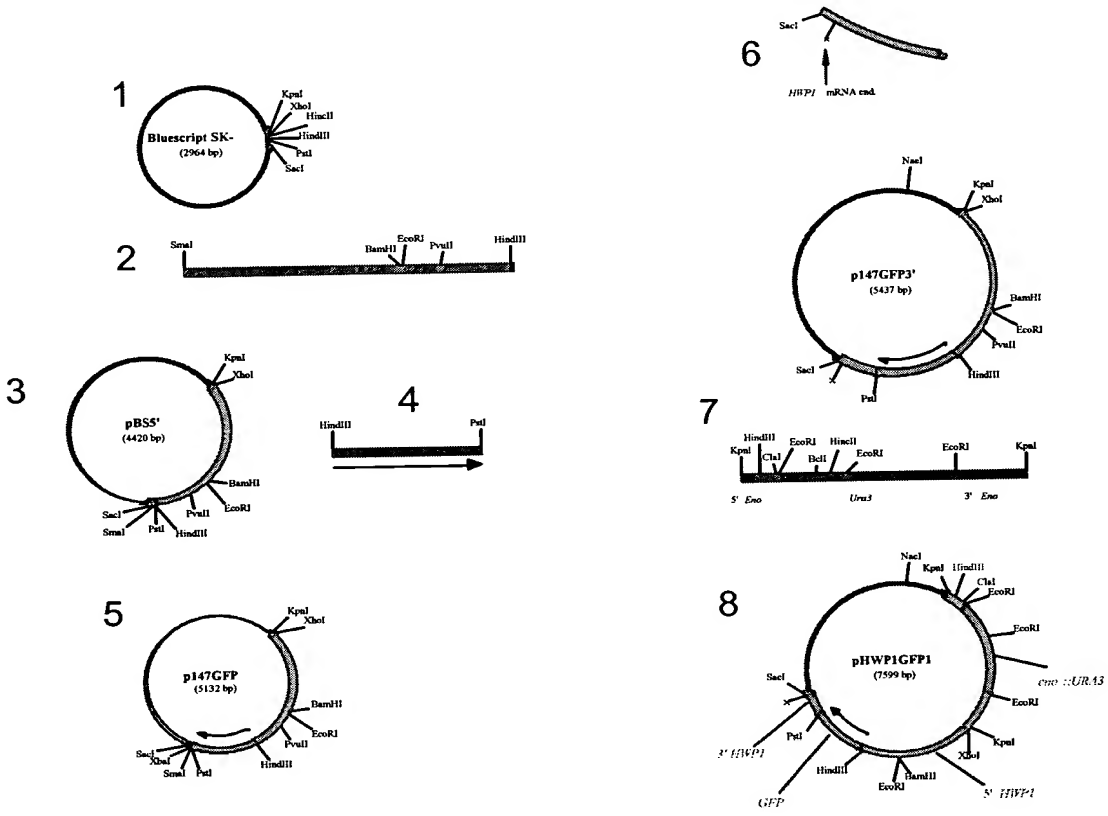
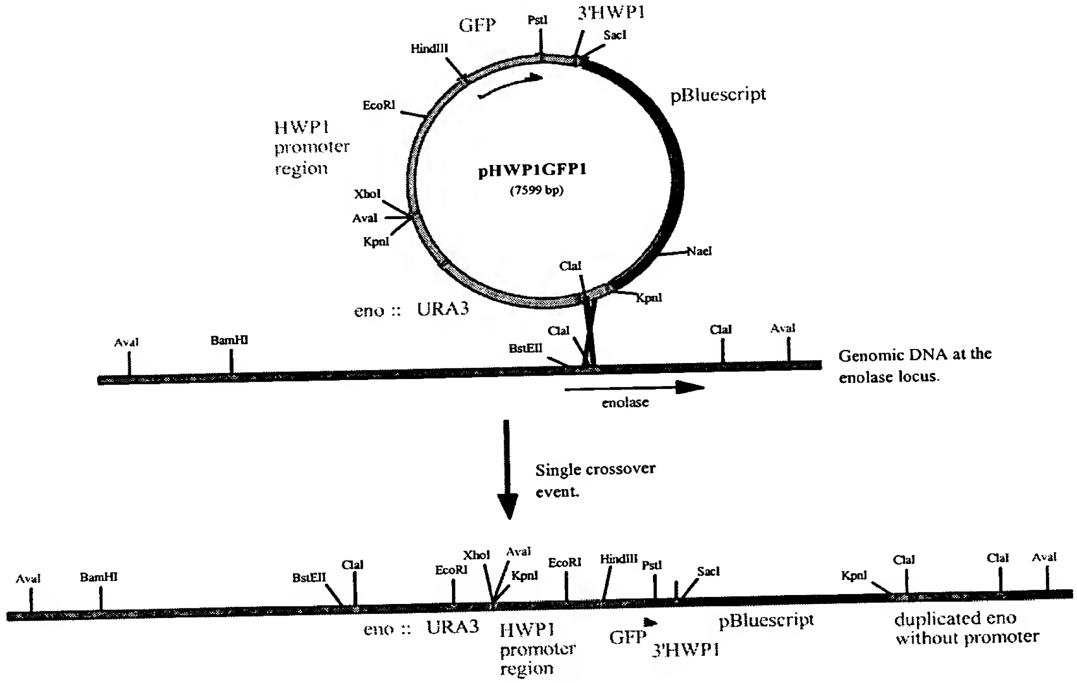

1
Bluescript SK-
(2964 bp)
KpnI
XhoI
HincII
HindIII
PstI
SacI
2
SmaI
BamHI
EcoRI
PvuII
HindIII
3
pBS5'
(4420 bp)
KpnI
XhoI
BamHI
EcoRI
PvuII
HindIII
PstI
SmaI
SacI
4
HindIII
PstI
5
p147GFP
(5132 bp)
KpnI
XhoI
BamHI
EcoRI
PvuII
HindIII
PstI
SmaI
XbaI
SacI
6
SacI
HWP1 mRNA end.
7
p147GFP3'
(5437 bp)
NaeI
KpnI
XhoI
BamHI
EcoRI
PvuII
HindIII
PstI
SacI
HindIII
KpnI
EcoRI
ClaI
HincII
BclI
EcoRI
EcoRI
KpnI
5' Eno
Ura3
3' Eno
8
pHWP1GFP1
(7599 bp)
NaeI
KpnI
HindIII
ClaI
EcoRI
EcoRI
eno ::URA3
EcoRI
KpnI
XhoI
BamHI
EcoRI
HindIII
PstI
SacI
3' HWP1
GFP
5' HWP1

Figure 8

Integration of pHWP1GFP1 into the chromosome of *C.albicans* at the enolase locus.



Integration of construct at the enolase locus.

Figure 9

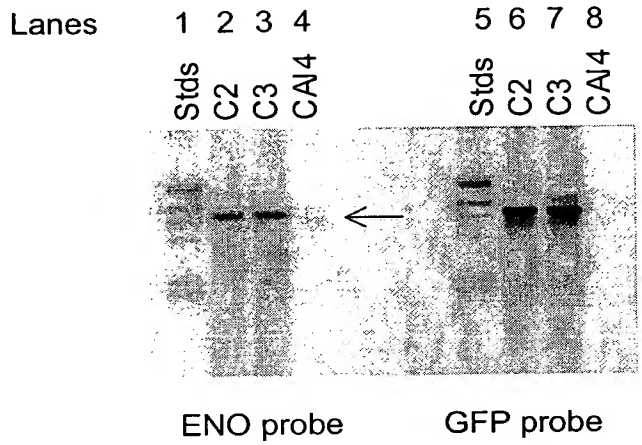


Figure 10

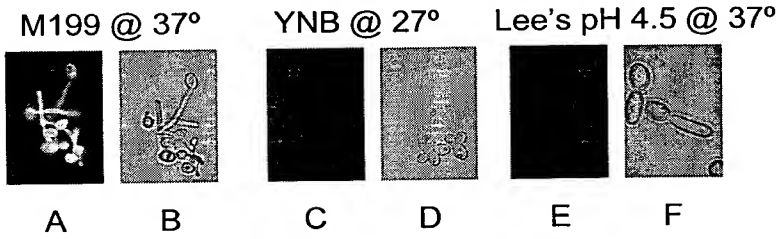
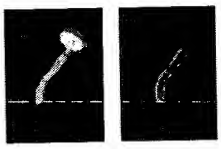


Figure 11



A B

Figure 12

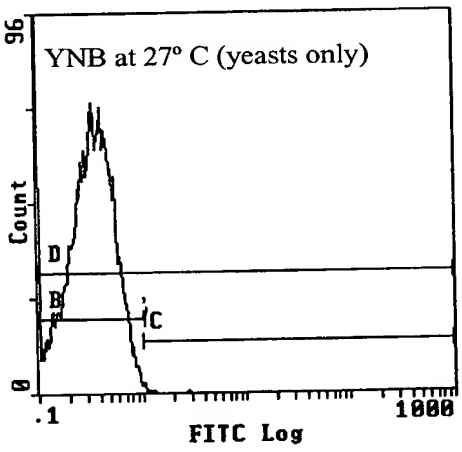


Figure 13A

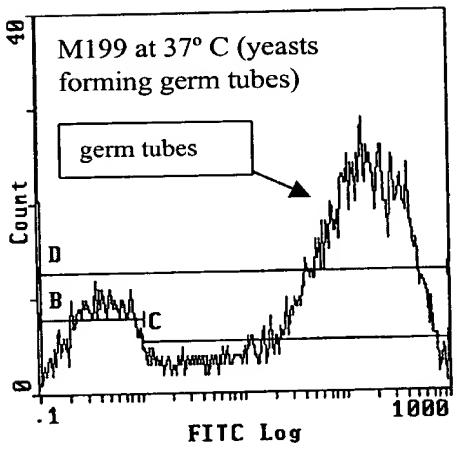


Figure 13B

5' GG **CTCGAG** GGA CCT TAC ACG CAC ATA AAT TGC Δ205 bp (SEQ ID. NO: 5)

5' GG **CTCGAG** CAA AAG TTA TTA GCG ATA ACC TGC Δ421 bp (SEQ ID. NO: 6)

5' GG **CTCGAG** GTG TAT TGT TCT CTT CAG TAC ATT Δ608 bp (SEQ ID. NO: 7)

5' GG **CTCGAG** CTC GAC TAA TCG ACT TTA CAT CAA Δ856 bp (SEQ ID. NO: 8)

5' GG **CTCGAG** ATG TCG ACT CAC AAT TCA TTG Δ1004 bp (SEQ ID. NO: 9)

5' GG **CTCGAG** GTT GCG ACT TTA ATA CCG TT Δ1209 bp (SEQ ID. NO: 10)

5' GG **CTCGAG** CAT AGC AAC TCT TGT AAA GTC Δ1271 bp (SEQ ID. NO: 11)

Figure 14A

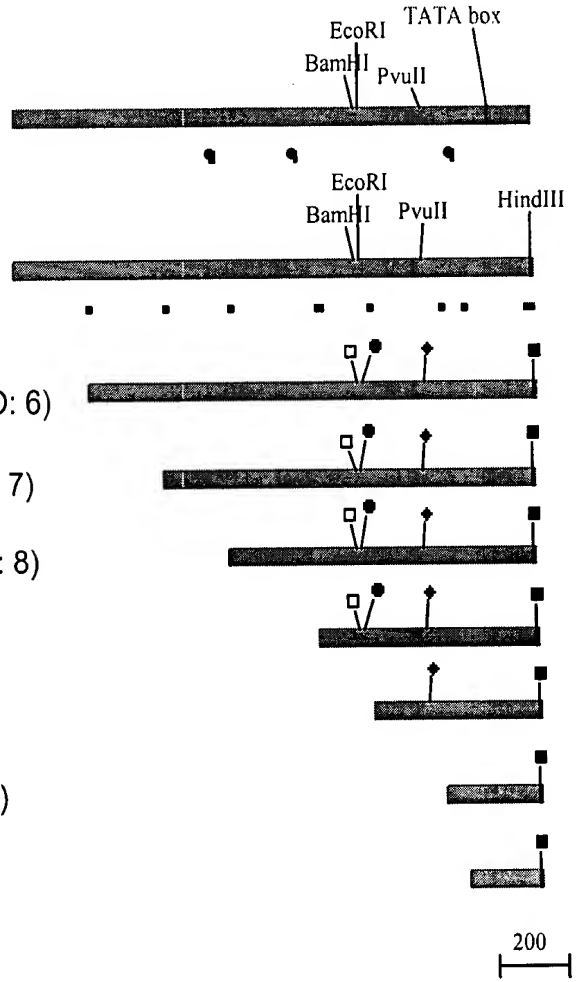


Figure 14B

Identification of virulence and morphogenesis factors in *C. albicans*

I. STEP 1: CREATE A GENOMIC LIBRARY FOR MICROARRAY CONSTRUCTION

Prepare *C. albicans* genomic DNA.

↓

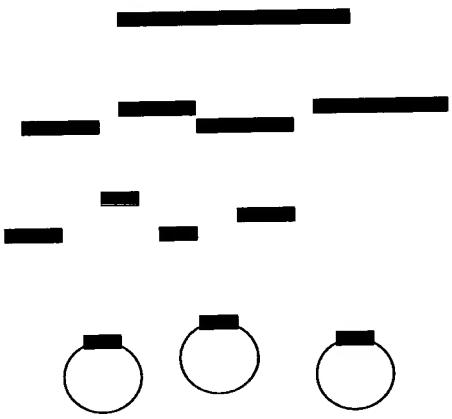
***Sau* 3A partial digest.**

↓

Size selection of 0.5 to 2.0 kb fragments.

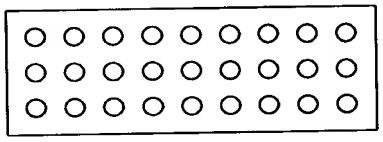
↓

Clone genomic fragments into plasmid vector (pBluescript).



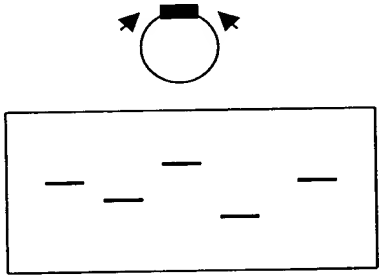
A. STEP 2: Create Microarray

Transfer transformants to 96-well plates.



↓

Perform colony PCR using universal primers.



↓

Check PCR rxns on gels and rearray positives on 96-well

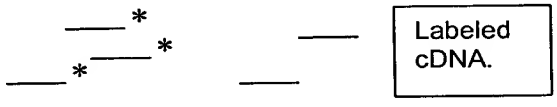
↓

Spot productive rxns on membranes.

↓

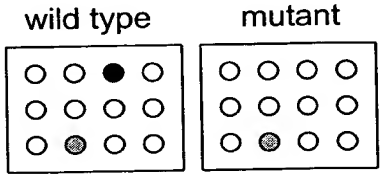
Prepare and label cDNA from mRNA of strains **with and without DNABPG**

Labeled cDNA from strain;
with DNABPG dnabpg null mutant



↓

Hybridize labeled cDNA to duplicate membranes.



↓

Go back to 96-well plates and sequence the clones of interest.

→ **In vivo analysis of genes.**

Figure 15